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- 1 -

SEQUENCE LISTING

<110> Gabriel Vogeli
Linda S. Wood

<120> G PROTEIN COUPLED RECEPTOR EXPRESSED IN BRAIN

<130> 28341/6202NCP

<140> US 09/634,109

<141> 2000-08-08

<150> US 09/377,563

<151> 2000-08-19

<160> 12

<170> PatentIn Ver. 2.0

<210> 1

<211> 948

<212> DNA

<213> Homo sapiens

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<221> CDS

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ggc atc ttt tcc cac agc cag act gac ctt gtc ctc ttc tct gca gtt	96
Gly Ile Phe Ser His Ser Gln Thr Asp Leu Val Leu Phe Ser Ala Val	
20 25 30	
atg gtg gtc ttc aca gtg gcc ctc tgt ggg aat gtc ctc ctc atc ttc	144
Met Val Val Phe Thr Val Ala Leu Cys Gly Asn Val Leu Leu Ile Phe	
35 40 45	
ctc atc tac ctg gac gct gga ctt cac acc ccc atg tac ttc ttc ctc	192
Leu Ile Tyr Leu Asp Ala Gly Leu His Thr Pro Met Tyr Phe Phe Leu	
50 55 60	
agc cag ctc tcc ctc atg gac ctc atg ttg gtc tgt aac att gtg cca	240
Ser Gln Leu Ser Leu Met Asp Leu Met Leu Val Cys Asn Ile Val Pro	
65 70 75 80	
aag atg gca gcc aac ttc ctg tct ggc agg aag tcc atc tcc ttt gtg	288
Lys Met Ala Ala Asn Phe Leu Ser Gly Arg Lys Ser Ile Ser Phe Val	
85 90 95	
ggc tgt ggc ata caa att ggc ttt ttt gtc tct ctt gtg gga tct gag	336
Gly Cys Gly Ile Gln Ile Gly Phe Phe Val Ser Leu Val Gly Ser Glu	
100 105 110	
ggg ctc ttg ctg gga ctc atg gct tat gac cac tac gtg gcc gtt agc	384
Gly Leu Leu Gly Leu Met Ala Tyr Asp His Tyr Val Ala Val Ser	
115 120 125	

cac cca ctt cac tat ccc atc ctc atg aat cag agg gtc tgt ctc cag 432
 His Pro Leu His Tyr Pro Ile Leu Met Asn Gln Arg Val Cys Leu Gln
 130 135 140
 att act ggg agc tcc tgg gcc ttt ggg ata ata gat gga gtg att cag 480
 Ile Thr Gly Ser Ser Trp Ala Phe Gly Ile Ile Asp Gly Val Ile Gln
 145 150 155 160
 atg gtg gca gcc atg ggc tta cct tac tgt ggc tca agg agc gtg gat 528
 Met Val Ala Ala Met Gly Leu Pro Tyr Cys Gly Ser Arg Ser Val Asp
 165 170 175
 cac ttt ttc tgt gag gta caa gct tta ttg aag ctg gcc tgt gca gac 576
 His Phe Phe Cys Glu Val Gln Ala Leu Leu Lys Leu Ala Cys Ala Asp
 180 185 190
 act tcc ctt ttt gac acc ctc ctc ttt gct tgc tgt gtc ttc atg ctt 624
 Thr Ser Leu Phe Asp Thr Leu Leu Phe Ala Cys Cys Val Phe Met Leu
 195 200 205
 ctc ctt ccc ttc tcc atc atc atg gcc tcc tat gct tgc atc cta ggg 672
 Leu Leu Pro Phe Ser Ile Ile Met Ala Ser Tyr Ala Cys Ile Leu Gly
 210 215 220
 gct gtg ctc cga ata cgc tct gct cag gcc tgg aaa aaa gcc ctg gcc 720
 Ala Val Leu Arg Ile Arg Ser Ala Gln Ala Trp Lys Lys Ala Leu Ala
 225 230 235 240
 acc tgc tcc tcc cac cta aca gct gtc acc ctc ttc tat ggg gca gcc 768
 Thr Cys Ser Ser His Leu Thr Ala Val Thr Leu Phe Tyr Gly Ala Ala
 245 250 255
 atg ttc atg tac ctg agg cct agg cgc tac cgg gcc cct agc cat gac 816
 Met Phe Met Tyr Leu Arg Pro Arg Arg Tyr Arg Ala Pro Ser His Asp
 260 265 270
 aag gtg gcc tct atc ttc tac aca gtc ctt act ccc atg ctg aac ccc 864
 Lys Val Ala Ser Ile Phe Tyr Thr Val Leu Thr Pro Met Leu Asn Pro
 275 280 285
 ctc att tac agc ttg agg aat ggg gag gtg atg ggg gca ctg agg aag 912
 Leu Ile Tyr Ser Leu Arg Asn Gly Glu Val Met Gly Ala Leu Arg Lys
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 ggg ctg gac cgc tgc agg att ggc agc cag cac tga 948
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 305 310 315

<210> 2
 <211> 315
 <212> PRT
 <213> Homo sapiens

<400> 2
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Met Val Val Phe Thr Val Ala Leu Cys Gly Asn Val Leu Leu Ile Phe

35 40 45

Leu Ile Tyr Leu Asp Ala Gly Leu His Thr Pro Met Tyr Phe Phe Leu
50 55 60

Ser Gln Leu Ser Leu Met Asp Leu Met Leu Val Cys Asn Ile Val Pro
65 70 75 80

Lys Met Ala Ala Asn Phe Leu Ser Gly Arg Lys Ser Ile Ser Phe Val
85 90 95

Gly Cys Gly Ile Gln Ile Gly Phe Phe Val Ser Leu Val Gly Ser Glu
100 105 110

Gly Leu Leu Leu Gly Leu Met Ala Tyr Asp His Tyr Val Ala Val Ser
115 120 125

His Pro Leu His Tyr Pro Ile Leu Met Asn Gln Arg Val Cys Leu Gln
130 135 140

Ile Thr Gly Ser Ser Trp Ala Phe Gly Ile Ile Asp Gly Val Ile Gln
145 150 155 160

Met Val Ala Ala Met Gly Leu Pro Tyr Cys Gly Ser Arg Ser Val Asp
165 170 175

His Phe Phe Cys Glu Val Gln Ala Leu Leu Lys Leu Ala Cys Ala Asp
180 185 190

Thr Ser Leu Phe Asp Thr Leu Leu Phe Ala Cys Cys Val Phe Met Leu
195 200 205

Leu Leu Pro Phe Ser Ile Ile Met Ala Ser Tyr Ala Cys Ile Leu Gly
210 215 220

Ala Val Leu Arg Ile Arg Ser Ala Gln Ala Trp Lys Lys Ala Leu Ala
225 230 235 240

Thr Cys Ser Ser His Leu Thr Ala Val Thr Leu Phe Tyr Gly Ala Ala
245 250 255

Met Phe Met Tyr Leu Arg Pro Arg Arg Tyr Arg Ala Pro Ser His Asp
260 265 270

Lys Val Ala Ser Ile Phe Tyr Thr Val Leu Thr Pro Met Leu Asn Pro
275 280 285

Leu Ile Tyr Ser Leu Arg Asn Gly Glu Val Met Gly Ala Leu Arg Lys
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Gly Leu Asp Arg Cys Arg Ile Gly Ser Gln His
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<210> 3

<211> 22

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: PRIMER
SEQUENCE

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<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence: PRIMER
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<210> 5
<211> 59
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PRIMER
SEQUENCE

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<210> 6
<211> 60
<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence: PRIMER
SEQUENCE

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<210> 7
<211> 9
<212> PRT
<213> Artificial Sequence

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<223> Description of Artificial Sequence: MAP KINASE
SUBSTRATE PEPTIDE

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<210> 8
<211> 316
<212> PRT
<213> Homo sapiens

<400> 8

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20 25 30

Tyr Leu Leu Thr Leu Val Gly Asn Thr Leu Ile Ile Leu Leu Ser Ala
35 40 45

Leu Asp Thr Lys Leu His Ser Pro Met Tyr Phe Phe Leu Ser Asn Leu
50 55 60

Ser Phe Leu Asp Leu Cys Phe Thr Thr Ser Cys Val Pro Gln Met Leu
65 70 75 80

Ala Asn Leu Trp Gly Pro Lys Lys Thr Ile Ser Phe Leu Asp Cys Ser
85 90 95

Val Gln Ile Phe Ile Phe Leu Ser Leu Gly Thr Thr Glu Cys Ile Leu
100 105 110

Met Lys Val Met Ala Phe Asp Arg Tyr Val Ala Val Cys Gln Pro Leu
115 120 125

His Tyr Ala Thr Ile Ile His Pro Arg Leu Cys Trp Gln Leu Ala Ser
130 135 140

Val Ala Trp Val Ile Gly Leu Val Gly Ser Val Val Gln Thr Pro Ser
145 150 155 160

Thr Leu His Leu Pro Phe Cys Pro Asp Arg Gln Val Asp Asp Phe Val
165 170 175

Cys Glu Val Pro Ala Leu Ile Arg Leu Ser Cys Glu Asp Thr Ser Tyr
180 185 190

Asn Glu Ile Gln Val Ala Val Ala Ser Val Phe Ile Leu Val Val Pro
195 200 205

Leu Ser Leu Ile Leu Val Ser Tyr Gly Ala Ile Thr Trp Ala Val Leu
210 215 220

Arg Ile Asn Ser Ala Thr Ala Trp Arg Lys Ala Phe Gly Thr Cys Ser
225 230 235 240

Ser His Leu Thr Val Val Thr Leu Phe Tyr Ser Ser Val Ile Ala Val
245 250 255

Tyr Leu Gln Pro Lys Asn Pro Tyr Ala Gln Gly Arg Gly Lys Phe Phe
260 265 270

Gly Leu Phe Tyr Ala Val Gly Thr Pro Ser Leu Asn Pro Leu Val Tyr
275 280 285

Thr Leu Arg Asn Lys Glu Ile Lys Arg Ala Leu Arg Arg Leu Leu Gly
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Lys Glu Arg Asp Ser Arg Glu Ser Trp Arg Ala Ala
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<210> 9
<211> 223
<212> PRT
<213> Mus musculus

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Gly Cys Gly Ile Gln Ile Gly Phe Phe Val Ser Leu Val Gly Ser Glu
35 40 45
Gly Leu Leu Leu Gly Leu Met Ala Tyr Asp Arg Tyr Val Ala Ile Ser
50 55 60
His Pro Leu His Tyr Pro Ile Leu Met Ser Gln Lys Val Cys Leu Gln
65 70 75 80
Ile Ala Gly Ser Ser Trp Ala Phe Gly Ile Leu Asp Gly Ile Ile Gln
85 90 95
Met Val Ala Ala Met Ser Leu Pro Tyr Cys Gly Ser Arg Tyr Ile Asp
100 105 110
His Phe Phe Cys Glu Val Pro Ala Leu Leu Lys Leu Ala Cys Ala Asp
115 120 125
Thr Ser Leu Phe Asp Thr Leu Leu Phe Ala Cys Cys Val Phe Met Leu
130 135 140
Leu Leu Pro Phe Ser Ile Ile Val Thr Ser Tyr Ala Arg Ile Leu Gly
145 150 155 160
Ala Val Leu Arg Met His Ser Ala Gln Ser Arg Lys Lys Ala Leu Ala
165 170 175
Thr Cys Ser Ser His Leu Thr Ala Val Ser Leu Phe Tyr Gly Ala Ala
180 185 190
Met Phe Ile Tyr Leu Arg Pro Arg Arg Tyr Arg Ala Pro Ser His Asp
195 200 205
Lys Val Val Ser Ile Phe Tyr Thr Val Leu Thr Pro Met Leu Asn
210 215 220

<210> 10
<211> 1070
<212> DNA
<213> Homo Sapiens

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ccatgggaag atgggtgaac cagtcctaca cagatggctt cttcctcttg ggcattcttt 180
cccacagcca gactgacctt gtcctcttct ctgcagttat ggtgggtcttc acagtggccc 240
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tgtacttctt cctcagccag ctctccctca tggacctcat gttgggtctgt aacattgtgc 360
caaagatggc agccaacttc ctgtctggca ggaagtccat ctctttgtg ggctgtggca 420
tacaaattgg cttttttgtc tctcttgtgg gatctgaggg gctcttgctg ggactcatgg 480

cttatgacca ctacgtggcc gttagccacc cacttcacta tcccatcctc atgaatcaga 540
 ggggtctgtct ccagattact gggagctcct gggcctttgg gataatagat ggagtgattc 600
 agatgggtggc agccatgggc ttaccttact gtggctcaag gagcgtggat cactttttct 660
 gtgaggtaca agctttattg aagctggcct gtgcagacac ttcccttttt gagaccctcc 720
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 ccacctgctc ctcccaccta acagctgtca ccctcttcta tggggcagcc atgttcctgt 900
 acctgagggc taggcgtac cgggccccta gccatgacaa ggtggcctct atcttctaca 960
 cagtccttac tcccatgctg aacccctca tttacagctt gaggaatggg gaggtgatgg 1020
 gggcactgag gaaggggctg gaccgctgca ggattggcag ccagcactga 1070

<210> 11

<211> 43

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:
 Oligonucleotide Primer

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<210> 12

<211> 50

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:
 Oligonucleotide Primer

<400> 12

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<210> 13

<211> 305

<212> PRT

<213> Homo sapiens

<400> 13

Asn Gln Ser Tyr Thr Asp Gly Phe Phe Leu Leu Gly Ile Phe Ser His
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Ser Gln Thr Asp Leu Val Leu Phe Ser Ala Val Met Val Val Phe Thr
 20 25 30

Val Ala Leu Cys Gly Asn Val Leu Leu Ile Phe Leu Ile Tyr Leu Asp
 35 40 45

Ala Gly Leu His Thr Pro Met Tyr Phe Phe Leu Ser Gln Leu Ser Leu
 50 55 60

Met Asp Leu Met Leu Val Cys Asn Ile Val Pro Lys Met Ala Ala Asn
 65 70 75 80

13
 cont'd

Phe Leu Ser Gly Arg Lys Ser Ile Ser Phe Val Gly Cys Gly Ile Gln
85 90 95

Ile Gly Phe Phe Val Ser Leu Val Gly Ser Glu Gly Leu Leu Leu Gly
100 105 110

Leu Met Ala Tyr Asp His Tyr Val Ala Val Ser His Pro Leu His Tyr
115 120 125

Pro Ile Leu Met Asn Gln Arg Val Cys Leu Gln Ile Thr Gly Ser Ser
130 135 140

Trp Ala Phe Gly Ile Ile Asp Gly Val Ile Gln Met Val Ala Ala Met
145 150 155 160

Gly Leu Pro Tyr Cys Gly Ser Arg Ser Val Asp His Phe Phe Cys Glu
165 170 175

Val Gln Ala Leu Leu Lys Leu Ala Cys Ala Asp Thr Ser Leu Phe Asp
180 185 190

Thr Leu Leu Phe Ala Cys Cys Val Phe Met Leu Leu Leu Pro Phe Ser
195 200 205

Ile Ile Met Ala Ser Tyr Ala Cys Ile Leu Gly Ala Val Leu Arg Ile
210 215 220

Arg Ser Ala Gln Ala Trp Lys Lys Ala Leu Ala Thr Cys Ser Ser His
225 230 235 240

Leu Thr Ala Val Thr Leu Phe Tyr Gly Ala Ala Met Phe Met Tyr Leu
245 250 255

Arg Pro Arg Arg Tyr Arg Ala Pro Ser His Asp Lys Val Ala Ser Ile
260 265 270

Phe Tyr Thr Val Leu Thr Pro Met Leu Asn Pro Leu Ile Tyr Ser Leu
275 280 285

Arg Asn Gly Glu Val Met Gly Ala Leu Arg Lys Gly Leu Asp Arg Cys
290 295 300

Arg
305

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<210> 14
 <211> 223
 <212> PRT
 <213> Homo sapiens

<400> 14

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 20 25 30

Gly Cys Gly Ile Gln Ile Gly Phe Phe Val Ser Leu Val Gly Ser Glu
 35 40 45

Gly Leu Leu Leu Gly Leu Met Ala Tyr Asp His Tyr Val Ala Val Ser
 50 55 60

His Pro Leu His Tyr Pro Ile Leu Met Asn Gln Arg Val Cys Leu Gln
 65 70 75 80

Ile Thr Gly Ser Ser Trp Ala Phe Gly Ile Ile Asp Gly Val Ile Gln
 85 90 95

Met Val Ala Ala Met Gly Leu Pro Tyr Cys Gly Ser Arg Ser Val Asp
 100 105 110

His Phe Phe Cys Glu Val Gln Ala Leu Leu Lys Leu Ala Cys Ala Asp
 115 120 125

Thr Ser Leu Phe Asp Thr Leu Leu Phe Ala Cys Cys Val Phe Met Leu
 130 135 140

Leu Leu Pro Phe Ser Ile Ile Met Ala Ser Tyr Ala Cys Ile Leu Gly
 145 150 155 160

Ala Val Leu Arg Ile Arg Ser Ala Gln Ala Trp Lys Lys Ala Leu Ala
 165 170 175

Thr Cys Ser Ser His Leu Thr Ala Val Thr Leu Phe Tyr Gly Ala Ala
 180 185 190

Met Phe Met Tyr Leu Arg Pro Arg Arg Tyr Arg Ala Pro Ser His Asp
 195 200 205

Lys Val Ala Ser Ile Phe Tyr Thr Val Leu Thr Pro Met Leu Asn
 210 215 220

A3
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